IN THE SPECIFICATION:

Please amend the paragraph beginning at page 20 line 20 as follows:

~~**Figure 3**~~**Figure 3A-3B(3)** is a representation of the nucleotide sequence and structure of the SOCS1 gene. A. The genomic context of SOCS1 in relation to the protamine gene cluster on murine chromosome 16. The accession number of this locus is MMPRMGNS (direct submission; G. Schlueter, 1995) for the mouse and BTPRMTNP2 for the rat (direct submission; G. Schlueter, 1996). B(1)-(3). The nucleotide sequence of the SOCS1 cDNA and deduced amino acid sequence. Conventional one letter abbreviations are used for the amino acid sequence and the asterisk indicates the stop codon. The polyadenylation signal sequence is underlined. The coding region is shown in uppercase and the untranslated region is shown in lower case.

Please amend the paragraph beginning at page 21, line 20 as follows:

~~**Figure 7**~~**Figure 7A-B** is a representation of protein extracts prepared from (7A) M1 cells or M1 cells expressing SOCS1 (4A2) and (7B) M1.mpl cells or M1.mpl.SOCS1 cells incubated for 10 min at 37°C in 10 ml serum-free DME containing either saline, 100 ng/ml IL-6 or 100 ng/ml IFN-γ. The binding reactions contained 4-6 μg protein (constant within a given experiment), 5 ng ^{32}P-labelled m67 oligonucleotide encoding the high affinity SIF (c-*sis*- inducible factor) binding site, and 800 ng sonicated salmon sperm DNA. For certain experiments, protein samples were preincubated with an excess of unlabelled m67 oligonucleotide, or antibodies specific for either STAT1 or STAT3.

Please amend the paragraph beginning at page 22, line 6 as follows:

~~**Figure 9**~~**Figure 9(I)-9(III)** is a representation of a comparison of the amino acid sequences of SOCS1, SOCS2, SOCS3 and CIS. Alignment of the predicted amino acid sequence of mouse (mm), human (hs) and rat (rr) SOCS1, SOCS2, SOCS3 and CIS. Those residues shaded are

conserved in three or four mouse SOCS family members. The SH2 domain is boxed in solid lines, while the SOCS box is bounded by double lines.

Please amend the paragraph beginning at page 22, line 16 as follows:

~~**Figure 11**~~**Figure 11A-11C** is a photographic representation showing expression of mRNA for SOCS family members *in vitro* and *in vivo*.

(11A) Northern analysis of mRNA from a range of mouse organs showing constitutive expression of SOCS family members in a limited number of tissues.

(11B) Norther analysis of mRNA from liver and M1 cells showing induction of expression of SOCS family members following exposure to IL-6.

(11C) Reverse transcriptase PCR analysis of mRNA from bone marrow showing induction of expression of SOCS family members by a range of cytokines.

Please amend the paragraph beginning at page 22, line 25 as follows:

~~**Figure 12**~~**Figure 12A-12B** is a photographic representation showing SOCS1 suppresses the phosphorylation and activation of gp130 and STAT-3.

(12A) Western blots of extracts from parental M1 cells (M1 and M1.mpl) and M1 cells expressing SOCS1 (4A2 and M1.mpl.SOCS1) stimulated with (+) or without (-) 100 ng/ml IL-6. Top: Extracts immunoprecipitated with antu-gp130 (αgp130) and immunoblotted with anti-phosphotyrosine (αPY-STAT3), or for STAT3 (αSTAT3) to demonstrate equal loading of protein. The molecular weights of the bands are shown on the right.

(12B) EMSA of M1.mpl and M1.mpl.SOCS1 cells stimulated with (+) and without (-) 100 ng/ml IL-6 or 100 ng/ml IFNγ. The DNA-binding complexes SIF A, B, and C are indicated at the left.

Please amend the paragraph beginning at page 23, line 5 as follows:

~~Figure 13~~**Figure 13A(i)-13F(ii)** is a representation of a comparison of the amino acid sequence of the SOCS proteins. (13A(i)-(ii)) Schematic representation of structures of SOCS proteins including proteins which contain WD-40 repeats (WSB) and ankyrin repeats (ASB). (13B(i)-(ii)) Alignment of N-terminal regions of SOCS proteins. (13C(i)-(ii)) Alignment of the SH2 domains of CIS, SOCS1, 2, 3, 5, 9, 11 and 14. (13D) Alignment of the WD-40 repeats of SOCS4, SOCS6, SOCS13 and SOCS15. (13E(i)-(ii)) Alignment of the ankyrin repeats of SOCS7 and SOCS10. (13F(i)-(ii)) Alignment of the regions between SH2, WD-40 and ankyrin repeats and the SOCS box. ~~(G) Alignment of the SOCS box.~~ In each case the conventional one letter abbreviations for amino acids are used, with X denoting residues of uncertain identity and OOO denoting the beginning and the end of contigs. Amino acid sequence obtained from conceptual translation of nucleic acid sequence derived from isolated cDNAs is shown in upper case while amino acid sequence obtained by conceptual translation of ESTs is shown in lower case and is approximate only. Conserved residues, defined as (LIVMA), (FYW), (DE), (QN), (C, S, T), (KRH), (PG) are shaded in the SH2 domain, WD-40 repeats, ankyrin repeats and the SOCS box. For the alignment of SH2 domains, WD-40 repeats and ankyrin repeats a consensus sequence is shown above. In each case this has been derived from examination of a large and diverse set of domains (Neer *et al,* 1994; Bork, 1993).

Please amend the paragraph beginning at page 31, line 4 as follows:

~~Figure 47A~~**Figure 47A(i)-(iv)** is a representation showing the nucleotide sequence covering the mouse SOCS15 gene derived from analysis the mouse BAC listed in Table 15.1. The nucleotides encoding the predicted coding region, beginning with the ATG and ending in the

stop codon are shown in upper case, while those encoding the predicted 5' untranslated region, the introns and the 3' untranslated region are shown in lower case. The relationship of mouse BAC to mouse and human ESTs contigs is illustrated in Figure 46.

Please amend the paragraph beginning at page 31, line 11 as follows:

Figure 47B is a representation showing the predicted amino acid sequence of mouse SOCS15 protein, derived from the nucleotide sequence in Figure ~~47A~~47A(i)-(iv). The SOCS box, which also shown in Figure 13 is underlined.

Please amend the paragraph beginning at page 31, line 15 as follows:

~~**Figure 48A**~~**Figure 48A(i)-(v)** is a representation showing the nucleotide sequence covering the human SOCS15 gene derived from analysis the human BAC listed in Table 15.2. The nucleotides encoding the predicted coding region, beginning with the ATG and ending in the stop codon are shown in upper case, while those encoding the predicted 5' untranslated region, the introns and the 3' untranslated region are shown in lower case. The relationship of the human BAC to mouse and human ESTs contigs is illustrated in Figure 46.

Please amend the paragraph beginning at page 31, line 21 as follows:

Figure 48B is a representation showing the predicted amino acid sequence of human SOCS15 protein, derived from the nucleotide sequence in Figure ~~48A~~48A(i)-(v). The SOCS box, which also shown in Figure 13 is underlined.

Please amend the paragraph beginning at page 70, line 4 as follows:

The SOCS1 PCR product was used as a probe to isolate homologous cDNAs from a mouse thymus cDNA library. The sequence of the cDNAs proved to be identical to the PCR product, suggesting that constitutive or over expression, rather than mutation, of the SOCS1 protein was sufficient for generating an IL-6-unresponsive phenotype. Comparison of the sequence of

SOCS1 cDNA with nucleotide sequence databases revealed that it was present on mouse and rat genomic DNA clones containing the protamine gene cluster found on mouse chromosome 16. Closer inspection revealed that the 1.4 kb SOCS1 sequence was not homologous to any of the protamine genes, but rather represented a previously unidentified open reading frame located at the extreme 3' end of these clones (Figure 3A-3B(1)-3)). There were no regions of discontinuity between the sequences of the SOCS1 cDNA and genomic locus, suggesting that SOCS1 is encoded by a single exon. In addition to the genomic clone containing the protamine genes, a series of murine and human expressed sequenced tags (ESTs) also revealed large blocks of nucleotide sequence identity to mouse SOCS1. The sequence information provided by the human ESTs allowed the rapid cloning of cDNAs encoding human SOCS1.

Please amend the paragraph beginning at page 70, line 19 as follows:

The mouse and rat SOCS1 gene encodes a 212 amino acid protein whereas the human SOCS1 gene encodes a 211 amino acid protein. Mouse, rat and human SOCS1 proteins share 95-99% amino acid identity (Figure 9(I)-(III)). A search of translated nucleic acid databases with the predicted amino acid sequence of SOCS1 showed that it was most related to a recently cloned cytokine-inducible immediate early gene product, CIS, and two classes of ESTs. Full length cDNAs from the two classes of ESTs were isolated and found to encode proteins of similar length and overall structure to SOCS1 and CIS. These clones were given the names SOCS2 and SOCS3. Each of the four proteins contains a central SH2 domain and a C-terminal region termed the SOCS motif. The SOCS1 proteins exhibit an extremely high level of amino acid sequence similarity (95-99% identity) amongst different species. However, the forms of the SOCS1, SOCS2, SOCS3 and CIS from the same animal, while clearly defining a new family of SH2-containing proteins, exhibited a lower amino acid identity. SOCS2 and CIS exhibit

approximately 38% amino acid identity, while the remaining members of the family share approximately 25% amino acid identity (Figure 9(I)-(III)). The coding region of the genes for SOCS1 and SOC3 appear to contain no introns while the coding region of the genes for SOCS2 and CIS contain one and two introns, respectively.

Please amend the paragraph beginning at page 72, line 9 as follows:

Phosphorylation of the cell surface receptor component gp130, the cytoplasmic tyrosine kinase JAK1 and the transcription factor STAT3 is thought to play a central role in IL-6 signal transduction. These events were compared in the parental M1 and M1.mpl cell lines and their SOCS1-expressing counterparts. As expected, gp130 was phosphorylated rapidly in response to IL-6 in both parental lines, however, this was reduced five- to ten-fold in the cell lines expressing SOCS1 (Figure 6). Likewise, STAT3 phosphorylation was also reduced by approximately ten-fold in response to IL-6 in those cell lines expressing SOCS1 (Figure 6). Consistent with a reduction in STAT3 phosphorylation, activation of specific STAT DNA binding complexes, as determined by electrophoretic mobility shift assay, was also reduced. Notably, there was a reduction in the formation of SIF-A (containing STAT3), SIF-B (STAT1/STAT3 heterodimer) and SIF-C (containing STAT1), the three STAT complexes induced in M1 cells stimulated with IL-6 (Figure 7A-B). Similarly, constitutive expression of SOCS1 also inhibited IFN-γ-stimulated formation of p91 homodimers (Figure 7A-B). STAT phosphorylation and activation were not the only cytoplasmic processes to be effected by SOCS1 expression, as the phosphorylation of other proteins, including shc and MAP kinase, was reduced to a similar extent (Figure 7A-B).

Please amend the paragraph beginning at page 77, line 16 as follows:

SOCS1, SOCS2 and SOCS3 are members of the SOCS protein family identified in Examples 1-16. Each contains a central SH2 domain and a conserved motif at the C-terminus, named the SOCS box. In order to isolate further members of this protein family, various DNA databases were searched with the amino acid sequence corresponding to conserved residues of the SOCS box. This search revealed the presence of human and mouse ESTs encoding twelve further members of the SOCS protein family (Figure 13A(i)-13F(ii)). Using this sequence information cDNAs encoding SOCS4, SOCS5, SOCS6, SOCS7, SOCS9, SOCS10, SOCS11, SOCS12, SOCS13, SOCS14 and SOCS15 have been isolated. Further analysis of contigs derived from ESTs and cDNAs revealed that the SOCS proteins could be placed into three groups according to their predicted structure N-terminal of the SOCS box. The three groups are those with (i) SH2 domains, (ii) WD-40 repeats and (iii) ankyrin repeats.

Please amend the paragraph beginning at page 78, line 4 as follows:

Eight SOCS proteins with SH2 domains have been identified. These include SOCS1, SOCS2 and SOCS3, SOCS5, SOCS9, SOCS11 and SOCS14 (Figure 13A(i)-13F(ii)). Full length cDNAs were isolated for mouse SOCS5 and SOCS14 and partial clones encoding mouse SOCS9 and SOCS14. Analysis of primary amino acid sequence and genomic structure suggest that pairs of these proteins (SOCS1 and SOCS3, SOCS2 and CIS, SOCS5 and SOCS14 and SOCS9 and SOCS11) are most closely related (Figure 13A(i)-13F(ii)). Indeed, the SH2 domains of SOCS5 and SOCS14 are almost identical (Figure 13B(i)-(ii)), and unlike CIS, SOCS1, SOCS2 and SOCS3, SOCS5 and SOCS14 have an extensive, though less well conserved, N-terminal region preceding their SH2 domains (Figure 13A(i)-(ii)).

Please amend the paragraph beginning at page 78, line 16 as follows:

Four SOCS proteins with WD-40 repeats were identified. As with the SOCS proteins with SH2 domains, pairs of these proteins appeared to be closely related. Full length cDNAs of mouse SOCS4 and SOCS6 were isolated and shown to encode proteins containing eight WD-40 repeats N-terminal of the SOCS box (Figure 13A(i)-13F(ii)) and SOCS4 and SOCS6 share 65% amino acid similarity. SOCS15 was recognised as an open reading frame upon sequencing BACs from human chromosome 12p13 and the syntenic region of mouse chromosome 6 [Ansari-Lari *et al,* 1997]. In the human, chimp and mouse, SOCS15 is encoded by a gene with two coding exons that lies within a few hundred base pairs of the 3' end of the triose phosphate isomerase (TPI) gene, but which is encoded on the opposite strand to TPI (9). In addition to a C-terminal SOCS box, the SOCS15 protein contains four WD-40 repeats. Interestingly, within the EST databases, there is a sequence of a nematode, an insect and a fish relative of SOCS15. SOCS15 appears most closely related to SOCS13.

Please amend the paragraph beginning at page 80, line 20 as follows:

Mouse and human SOCS5 were recognized through searching EST databases using the SOCS box consensus (Figure 13A(i)-13F(ii)). Those ESTs derived from mouse and human SOCS5 cDNAs are tabulated below (Tables 5.1 and 5.2). Using sequence information derived from mouse and human ESTs, several oligonucleotides were designed and used to screen, in the conventional manner, a mouse thymus cDNA library, a mouse genomic DNA library and a human thymus cDNA library cloned into λ-bacteriophage . A single genomic DNA clone (57-2) and (5-3-2) cDNA clone encoding mouse SOCS5 were isolated and sequenced in their entirety and shown to overlap with the mouse ESTs identified in the database (Figures 19 and 20A). The entire coding region, in addition to a region of 5' and 3' untranslated regions of mouse SOCS5

appears to be encoded on a single exon (Figure 19). Analysis of the sequence (Figure 20) confirms that SOCS5 genomic and cDNA clones encode a protein with a SOCS box at its C-terminus in addition to an SH2 domain (Figure 19 and 20B). The relationship of the human SOCS5 contig (h5.1; Figure 21) derived from analysis of cDNA clone 5-94-2 and the human SOCS5 ESTs (Table 5.2) to the mouse SOCS5 DNA sequence is shown in Figure 19. The nucleotide sequence and corresponding amino acid sequence of murine SOCS5 are shown in SEQ ID NOs: 17 and 18, respectively. The human SOCS5 nucleotide sequence is shown in SEQ ID NO:19.

Please amend the paragraph beginning at page 81, line 9 as follows:

Mouse and human SOCS6 were recognized through searching EST databases using the SOCS box consensus (Figure 13A(i)-13F(ii)). Those ESTs derived from mouse and human SOCS6 cDNAs are tabulated below (Tables 6.1 and 6.2). Using sequence information derived from mouse ESTs, several oligonucleotides were designed and use to screen, in the conventional manner, a mouse thymus cDNA library. Eight cDNA clones (6-1A, 6-2A, 6-5B, 6-4N, 6-18, 6-29, 6-3N, 6-5N) cDNA clone encoding mouse SOCS6 were isolated and sequenced in their entirety and shown to overlap with the mouse ESTs identified in the database (Figures 22 and 23A). Analysis of the sequence (Figure 23) confirms that the mouse SOCS6 cDNA clones encode a protein with a SOCS box at its C-terminus in addition to a eight WD-40 repeats (Figures 22 and 23B). The relationship of the human SOCS-6 contigs (h6.1 and h6.2 ; Figure 24) derived from analysis of human SOCS6 ESTs (Table 6.2) to the mouse SOCS6 DNA sequence is shown in Figure 22. The nucleotide and corresponding amino acid sequences of murine SOCS6 are shown in SEQ ID NOs: 20 and 21, respectively. SOCS6 human contigs h6.1 and h6.2 are shown in SEQ ID NOs: 22 and 23, respectively.

Please amend the paragraph beginning at page 81, line 27 as follows:

Mouse and human SOCS7 were recognized through searching EST databases using the SOCS box consensus (Figure 13A(i)-13F(ii)). Those ESTs derived from mouse and human SOCS-7 cDNAs are tabulated below (Tables 7.1 and 7.2). Using sequence information derived from mouse ESTs, several oligonucleotides were designed and use to screen, in the conventional manner, a mouse thymus cDNA library. One cDNA clone (74-10A-11) cDNA clone encoding mouse SOCS7 was isolated and sequenced in its entirety and shown to overlap with the mouse ESTs identified in the database (Figures 25 and 26A). Analysis of the sequence (Figure 26) suggests that mouse SOCS7 encodes a protein with a SOCS box at its C-terminus, in addition to several ankyrin repeats (Figure 25 and 26B). The relationship of the human SOCS7 contigs (h7.1 and h7.2 ; Figure 27) derived from analysis of human SOCS7 ESTs (Table 7.2) to the mouse SOCS7 DNA sequence is shown in Figure 25. The nucleotide and corresponding amino acid sequences of murine SOCS7 are shown in SEQ ID NOs: 24 and 25, respectively. The nucleotide sequence of SOCS7 human contigs h7.1 and h7.2 are shown in SEQ ID NOs: 26 and 27, respectively.

Please amend the paragraph beginning at page 82, line 24 as follows:

Mouse and human SOCS-9 were recognized through searching EST databases using the SOCS box consensus (Figure 13A(i)-13F(ii)). Those ESTs derived from mouse and human SOCS9 cDNAs are tabulated below (Tables 9.1 and 9.2). The relationship of the mouse SOCS9 contigs (m9.1; Figure 9.2) derived from analysis of the mouse SOCS9 EST (Table 9.1) to the human SOCS-9 DNA contig (h9.1; Figure 32) derived from analysis of human SOCS9 ESTs (Table 9.2) is shown in Figure 31. Analysis of the sequence (Figure 32) indicates that the human SOCS9 cDNA encodes a protein with a SOCS box at its C-terminus, in addition to an SH2 domain

(Figure 30). The nucleotide sequence of muring SOCS9 cDNA is shown in SEQ ID NO:30. The nucleotide sequence of human SOCS9 cDNA is shown in SEQ ID NO:31.

Please amend the paragraph beginning at page 83, line 6 as follows:

Mouse and human SOCS10 were recognized through searching EST databases using the SOCS box consensus (Figure 13A(i)-13F(ii)). Those ESTs derived from mouse and human SOCS10 cDNAs are tabulated below (Table 10.1 and 10.2). Using sequence information derived from mouse ESTs, several oligonucleotides were designed and use to screen, in the conventional manner, a mouse thymus cDNA library. Four cDNA clones (10-9, 10-12, 10-23 and 10-24) encoding mouse SOCS10 were isolated, sequenced in their entirety and shown to overlap with the mouse and human ESTs identified in the database (Figures 33 and 34). Analysis of the sequence (Figure 34) indicates that the mouse SOCS10 cDNA clone is not full length but that it does encode a protein with a SOCS box at its C-terminus, in addition to several ankyrin repeats (Figure 33). The relationship of the human SOCS10 contigs (h10.1 and h10.2; Figure 35) derived from analysis of human SOCS10 ESTs (Table 10.2) to the mouse SOCS10 DNA sequence is shown in Figure 33. Comparison of mouse cDNA clones and ESTs with human ESTs suggests that the 3' untranslated regions of mouse and human SOCS10 differ significantly. The nucleotide sequence of murine SOCS10 is shown in SEQ ID NO:32 and the nucleotide sequence of SOCS10 human contigs h10.1 and h10.2 are shown in SEQ ID NOs:33 and 34, respectively.

Please amend the paragraph beginning at page 83, line 25 as follows:

Human SOCS11 were recognized through searching EST databases using the SOCS box consensus (Figure 13A(i)-13F(ii)). Those ESTs derived from human SOCS11 cDNAs are tabulated below (Table 11.1 and 11.2). The relationship of the human SOCS11 contigs (h11.1;

Figure 36A, B), derived from analysis ESTs (Table 11.2) to the predicted encoded protein, is shown in Figure 37. Analysis of the sequence indicates that the human SOCS11 cDNA encodes a protein with a SOCS box at its C-terminus, in addition to an SH2 domain (Figure 37 and 36B). The nucleotide sequence and corresponding amino acid sequence of human SOCS11 are represented in SEQ ID NOs:35 and 36, respectively.

Please amend the paragraph beginning at page 84, line 6 as follows:

Mouse and human SOCS-12 were recognized through searching EST databases using the SOCS box consensus (Figure 13A(i)-13F(ii)). Those ESTs derived from mouse and human SOCS12 cDNAs are tabulated below (Tables 12.1 and 12.2). Using sequence information derived from mouse ESTs, several oligonucleotides were designed and use to screen, in the conventional manner, a mouse thymus cDNA library. Four cDNA clones (10-9, 10-12, 10-23 and 10-24) encoding mouse SOCS12 were isolated, sequenced in their entirety and shown to overlap with the mouse and human ESTs identified in the database (Figures 38 and 39). Analysis of the sequence (Figure 39 and 40) indicates that the SOCS12 cDNA clone encodes a protein with a SOCS box at its C-terminus, in addition to several ankyrin repeats (Figure 38). The relationship of the human SOCS12 contigs (h12.1 and h12.2; Figure 40) derived from analysis of human SOCS12 ESTs (Table 12.2) to the mouse SOCS12 DNA sequence is shown in Figure 38. Comparison of mouse cDNA clones and ESTs with human ESTs suggests that the 3' untranslated regions of mouse and human SOCS12 differ significantly. The nucleotide sequence of SOCS12 is shown in SEQ ID NO:37. The nucleotide sequence of human SOCS12 contigs h12.1 and h12.2 are shown in SEQ ID NOs:38 and 39, respectively.

Please amend the paragraph beginning at page 84, line 25 as follows:

Mouse and human SOCS-13 were recognized through searching EST databases using the SOCS box consensus (Figure 13A(i)-13F(ii)). Those ESTs derived from mouse and human SOCS13 cDNAs are tabulated below (Tables 13.1 and 13.2). Using sequence information derived from mouse ESTs, several oligonucleotides were designed and use to screen, in the conventional manner, a mouse thymus and a mouse embryo cDNA library. Three cDNA clones (62-1, 62-6-7 and 62-14) encoding mouse SOCS13 were isolated, sequenced in their entirety and shown to overlap with the mouse ESTs identified in the database (Figure 41 and 42A). Analysis of the sequence (Figure 42A-B) indicates that the mouse SOCS13 cDNA encodes a protein with a SOCS box at its C-terminus, in addition to a potential WD-40 repeat (Figure 41 and 42B). The relationship of the human SOCS13 contigs (h13.1 and h13.2; Figure 43) derived from analysis of human SOCS13 ESTs (Table 13.2) to the mouse SOCS13 DNA sequence is shown in Figure 41. The nucleotide sequence and corresponding amino acid sequence of murine SOCS13 and shown in SEQ ID NOs:40 and 41, respectively. The nucleotide sequence of human SOCS13 contig h13.1 is shown in SEQ ID NO:42.

Please amend the paragraph beginning at page 85, line 12 as follows:

Mouse and human SOCS-14 were recognized through searching EST databases using the SOCS box consensus (Figure 13A(i)-13F(ii)). Those ESTs derived from mouse and human SOCS14 cDNAs are tabulated below (Tables 14.1 and 14.2). Using sequence information derived from mouse and human ESTs, several oligonucleotides were designed and use to screen, in the conventional manner, a mouse thymus cDNA library, a mouse genomic DNA library and a human thymus cDNA library cloned into λ-bacteriophage . A single genomic DNA clone (57-2) and (5-3-2) cDNA clone encoding mouse SOCS14 were isolated and sequenced in their entirety

and shown to overlap with the mouse ESTs identified in the database (Figures 44 and 45A). The entire coding region, in addition to a region of 5' and 3' untranslated regions, of mouse SOCS14 appears to be encoded on a single exon (Figure 44). Analysis of the sequence (Figure 45A-B) confirms that SOCS14 genomic and cDNA clones encode a protein with a SOCS box at its C-terminus in addition to an SH2 domain (Figure 44 and 45B). The relationship of the human SOCS14 contig (h14.1; Figure 14.3) derived from analysis of cDNA clone 5-94-2 and the human SOCS14 ESTs (Table 14.2) to the mouse SOCS14 DNA sequence is shown in Figure 44.

Please amend the paragraph beginning at page 86, line 4 as follows:

Mouse and human SOCS15 were recognized through searching DNA databases using the SOCS box consensus (Figure 13A(i)-13F(ii)). Those ESTs derived from mouse and human SOCS15 cDNAs are tabulated below (Tables 15.1 and 15.2), as are a mouse and human BAC that contain the entire mouse and human SOCS-15 genes. Using sequence information derived from the ESTs and the BACs it is possible to predict the entire amino acid sequence of SOCS15 and as described for the other SOCS genes it is feasible to design specific oligonucleotide probes to allow cDNAs to be isolated. The relationship of the BACs to the ESTs is shown in Figure 46 and the nucleotide and predicted amino acid sequence of the SOCS-15, derived from the mouse and human BACs is shown in Figures 47A(i)-47B and 48A(i)-48B. The nucleotide sequence and corresponding amino acid sequence of murine SOCS15 are shown in SEQ ID NOs:46 and 47, respectively. The nucleotide and corresponding amino acid sequence of human SOCS15 are shown in SEQ ID NO:48 and 49, respectively.